

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds
(without alignments)
572.596 Million cell updates/sec

Title: US-10-761-557-3
Perfect score: 19
Sequence: 1 gcagaatggacgctaat 19

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : EST:
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_htc: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_est7: *
9: gb_gss1: *
10: gb_gss2: *
11: gb_gss3: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	DB ID	Description
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No matches found

Search completed: February 5, 2006, 13:07:28
Job time : 1552.5 secs

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OM nucleic - nucleic search, using sw model
 Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds
 (without alignments)
 1208.082 Million cell updates/sec

Title: US-10-761-557-3
 Perfect score: 19
 Sequence: 1 gcagaatggacgctaat 19

Scoring table: OLIGO_NUC
 Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : GenBank:
 1: gb_ba:
 2: gb_in:
 3: gb_env:
 4: gb_om:
 5: gb_ov:
 6: gb_pat:
 7: gb_ph:
 8: gb_pr:
 9: gb_ro:
 10: gb_sts:
 11: gb_sy:
 12: gb_un:
 13: gb_vl:
 14: gb_hg:
 15: gb_pl:
 16: gb_sg:
 17: gb_sg2:
 18: gb_sg3:
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 21: gb_sg6:
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 715: gb_sg700:
 716: gb_sg701:
 717: gb_sg702:
 718: gb_sg703:
 719: gb_sg704:
 720: gb_sg705:
 721: gb_sg706:
 722: gb_sg707:
 723: gb_sg708:
 724: gb_sg709:
 725: gb_sg710:
 726: gb_sg711:
 727: gb_sg712:
 728: gb_sg713:
 729: gb_sg714:
 730: gb_sg715:
 731: gb_sg716:
 732: gb_sg717:
 733: gb_sg718:
 734: gb_sg719:
 735: gb_sg720:
 736: gb_sg721:
 737: gb_sg722:
 738: gb_sg723:
 739: gb_sg724:
 740: gb_sg725:
 741: gb_sg726:
 742: gb_sg727:
 743: gb_sg728:
 744: gb_sg729:
 745: gb_sg730:
 746: gb_sg731:
 747: gb_sg732:
 748: gb_sg733:
 749: gb_sg734:
 750: gb_sg735:
 751: gb_sg736:
 752: gb_sg737:
 753: gb_sg738:
 754: gb_sg739:
 755: gb_sg740:
 756: gb_sg741:
 757: gb_sg742:
 758: gb_sg743:
 759: gb_sg744:
 760: gb_sg745:
 761: gb_sg746:
 762: gb_sg747:
 763: gb_sg748:
 764: gb_sg749:
 765: gb_sg750:
 766: gb_sg751:
 767: gb_sg752:
 768: gb_sg753:
 769: gb_sg754:
 770: gb_sg755:
 771: gb_sg756:
 772: gb_sg757:
 773: gb_sg758:
 774: gb_sg759:
 775: gb_sg760:
 776: gb_sg761:
 777: gb_sg762:
 778: gb_sg763:
 779: gb_sg764:
 780: gb_sg765:<br

GenCore version 5.1.6
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Om nucleic - nucleic search, using sw model

Run on: February 5, 2006, 07:35:28 i Search time 218.5 Seconds
(without alignments) 573.538 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggtaactaat 19

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1
Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : N_Geneseqn21:*

- 1: geneseqn1980s:*
- 2: geneseqn1980s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001a:*
- 5: geneseqn2001b:*
- 6: geneseqn2002a:*
- 7: geneseqn2002b:*
- 8: geneseqn2003a:*
- 9: geneseqn2003b:*
- 10: geneseqn2003c:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004a:*
- 13: geneseqn2004b:*
- 14: geneseqn2005:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB	ID	Description
1	19	100.0	19	13	ADT26144	Adt26144 sirNA C f

ALIGNMENTS

RESULT 1
ADT26144
ID ADT26144 standard; RNA; 19 BP.

XX

AC ADT26144;

XX DT 27-JAN-2005 (first entry)

XX DB sirNA C for potassium channel subunit Kv3.4.

XX KW RNA interference; gene silencing; ds; potassium channel;

KW fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;
sirNA; small interfering RNA; neurological condition; epilepsy; hearing;

KW learning and memory disorder.
OS Rattus rattus.

XX PN US2004220082-A1.

XX PD 04-NOV-2004.

XX PF 21-JAN-2004; 2004US-00761557.

XX PR 21-JAN-2003; 2003US-0441375P.

XX PA (NOUN) UNIV NORTHWESTERN.

XX PI Surmeier DJ, Tkatch T, Baranaukas G;
WPI; 2004-774947/76.

XX PT Inhibiting the ability of a fast-spiking neuronal cell to discharge at a high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's disease and other neurological conditions.

XX XX Example 6; SEQ ID NO 3; 27pp; English.

XX PS The invention relates to inhibiting the ability of a fast-spiking neuronal cell to discharge at a high rate comprising providing a compound capable of inhibiting Kv3.4 activity (potassium channel subunit) to a cell expressing Kv3 channels comprising a Kv3.4 subunit (especially the Kv3.4a subunit), where the high rate of discharge is inhibited. Also included are a method of manipulating neuronal ion channels (comprising transfecting a fast-spiking neuronal cell with a vector encoding an siRNA (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a composition comprising an siRNA construct capable of inhibiting expression of a Kv3.4 subunit in a neuronal cell and a method for screening for compounds that inhibit the activity of a Kv3.4 protein (comprising providing a cell expressing Kv3.4 protein, and a test compound, and detecting the activity of the Kv3.4 protein in the presence of the test compound). The method is useful for manipulating ion channels, in particular for treating Parkinson's disease and other neurological conditions, such as epilepsy, hearing, learning and memory disorders. The present sequence is an siRNA targeting nucleotides 1626-1644 (relative to the start codon) of the rat Kv3.4 mRNA.

XX XX SQ Sequence 19 BP: 6 A; 3 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.07%;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCAGATGGTGACGCTAAT 19

Db 1 GCAGATGGTGACGCTAAT 19

Search completed: February 5, 2006, 11:31:35
Job time : 218.5 sec

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds

(without alignments)
469.079 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggacgctaat 19

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PICTUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description

No matches found

Search completed: February 5, 2006, 12:04:00
Job time : 72 secs

Copyright (c) 1993 - 2006 Compugen Ltd.
 OM nucleic - nucleic search, using sw model
 Run on: February 5, 2006, 11:21:57 ; Search time 344.5 Seconds
 (without alignments)
 456.076 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagaatggacgtaat 19

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA_Main:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	19	100.0	19 8 US-10-761-557-3	Sequence 3, Appli

ALIGNMENTS

RESULT	1
US-10-761-557-3	
Sequence 3, Application US-10761557	
Publication No. US20040220082A1	
GENERAL INFORMATION:	
APPLICANT: Surmeier, D. James	
APPLICANT: Tkatch, Tatiana	
APPLICANT: Baranaukas, Gytis	
TITLE OF INVENTION: Manipulation of Neuronal Ion Channels	
FILE REFERENCE: NWESTRN-08739	
CURRENT APPLICATION NUMBER: US-10-761-557	
CURRENT FILING DATE: 2004-01-21	
NUMBER OF SEQ ID NOS: 5	
SOFTWARE: PatentIn version 3.2	
SEQ ID NO 3	
LENGTH: 19	
TYPE: DNA	

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OM nucleic - nucleic search, using bw model

Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds
(without alignments)

86.540 Million cell updates/sec

Title: US-10-761-557-3

Perfect score: 19

Sequence: 1 gcagatggacgctaat 19

Scoring table: OLIGO_NUC

Gapext 60.0 , Gapext 60.0

Searched: 6068529 seqs, 419036697 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA_New:*

1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
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No matches found

Search completed: February 5, 2006, 13:13:41
Job time : 184 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
 Run on: February 5, 2006, 11:29:11 ; Search time 1552.5 Seconds
 (without alignments) 572.596 Million cell updates/sec

Title: US-10-761-557-4
 Perfect score: 19
 Sequence: 1 ggcagtgtggccggaaac 19
 Scoring table: OLIGO NUC
 Gapop 60.0 , Gapext 60.0
 Searched: 41078325 seqs, 23393541228 residues
 Word size : 19
 Total number of hits satisfying chosen parameters: 0
 Minimum DB seq length: 0
 Maximum DB seq length: 19
 Post-processing: Listing first 100 summaries
 Database : EST:
 1: 9b_est1:
 2: 9b_est2:
 3: 9b_est3:
 4: 9b_htc:
 5: 9b_est4:
 6: 9b_est5:
 7: 9b_est6:
 8: 9b_est7:
 9: 9b_gss1:
 10: 9b_gss2:
 11: 9b_gss3:
 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
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No matches found

Search completed: February 5, 2006, 13:07:28
 Job time : 1552.5 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using bw model
Run on: February 5, 2006, 10:42:21 ; Search time 894 Seconds
(without alignments)
1208.082 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggccatgttggccggaaac 19

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : GenEmbl:
1: 9b_ba:
2: 9b_in:
3: 9b_env:
4: 9b_om:
5: 9b_ov:
6: 9b_jpat:
7: 9b_ph:
8: 9b_pr:
9: 9b_ro:
10: 9b_sts:
11: 9b_sy:
12: 9b_an:
13: 9b_vl:
14: 9b_btq:
15: 9b_pl:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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No matches found

Search completed: February 5, 2006, 12:01:29
Job time : 894 secs

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KW learning and memory disorder.
 XX Rattus rattus.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 07:35:28 ; Search time 218.5 Seconds
 (without alignments)
 579.538 Million cell updates/sec

Title: US-10-761-557-4

Perfect score: 19

Sequence: 1 ggcagtgtgagccaaac 19

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : N_Geneseqn21:
 1: geneseqn1980s:
 2: geneseqn1980s:
 3: geneseqn2000s:
 4: geneseqn2001as:
 5: geneseqn2001bs:
 6: geneseqn2002as:
 7: geneseqn2002bs:
 8: geneseqn2003as:
 9: geneseqn2003bs:
 10: geneseqn2003cs:
 11: geneseqn2003ds:
 12: geneseqn2004as:
 13: geneseqn2004bs:
 14: geneseqn2005s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	19	100.0	19	13	ADT26145

Adt26145 sirNA D f

ALIGNMENTS

RESULT 1					
ID	ADT26145	standard	RNA	19 BP.	
XX	XX	AC	ADT26145;		
XX	XX	DT	27-JAN-2005	(first entry)	
XX	XX	DE	DE sirNA D for potassium channel subunit Kv3.4.		

KW RNA interference; gene silencing; ds: potassium channel;
 KW fast spiking neuron; Parkinson's disease; Kv3.4; neuronal ion channel;
 KW siRNA; small interfering RNA; neurological condition; epilepsy; hearing;

KW learning and memory disorder.
 XX Rattus rattus.

OS US2004220082-A1.

PN 04-NOV-2004.

PR 21-JAN-2004; 2004US-00761557.

XX 21-JAN-2003; 2003US-0441375P.

PA (NOUN) UNIV NORTHWESTERN.

XX Surmeier DJ, Tkatch T, Baranuskas G;

PI XX WPI; 2004-774947/76.

XX Inhibiting the ability of a fast-spiking neuronal cell to discharge at a high rate by inhibiting Kv3.4 activity, useful for treating Parkinson's disease and other neurological conditions.

XX Example 6; SEQ ID NO 4; 27pp; English.

XX PS XX

CC The invention relates to inhibiting the ability of a fast-spiking

CC neuronal cell to discharge at a high rate comprising providing a compound

CC capable of inhibiting Kv3.4 activity (potassium channel subunit) to a

CC cell expressing Kv3.4 subunit (especially the Kv3.4a subunit), where the high rate of discharge is inhibited. Also

CC included are a method of manipulating neuronal ion channels (comprising

CC transfecting a fast-spiking neuronal cell with a vector encoding an siRNA (small interfering RNA) directed against an mRNA encoding a Kv3.4 protein

CC where the siRNA is capable of inhibiting Kv3.4 expression in the cell), a

CC composition comprising an siRNA construct capable of inhibiting

CC expression of a Kv3.4 subunit in a neuronal cell and a method for

CC screening for compounds that inhibit the activity of a Kv3.4 protein

CC (comprising providing a cell expressing Kv3.4 protein, and a test

CC compound, and detecting the activity of the Kv3.4 protein in the presence

CC of the test compound). The method is useful for manipulating ion

CC channels, in particular for treating Parkinson's disease and other

CC neurological conditions, such as epilepsy, hearing, learning and memory

CC disorders. The present sequence is an siRNA targeting nucleotides 11825-

XX 1843 (relative to the start codon) of the rat Kv3.4 mRNA.

XX Sequence 19 BP: 5' A; 4' C; 7' G; 3' T; 0' U; 0' Other;

XX Query Match 100.0%; Score 19; DB 13; Length 19;

XX Best Local Similarity 100.0%; Pred. No. 0.16%;

XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Qy 1 GGCAGTGTGAGCCGAAAC 19

Db 1 GGCAGTGTGAGCCGAAAC 19

Search completed: February 5, 2006, 11:31:35
 Job time : 218.5 secs

Copyright (c) 1993 - 2006 Compugen Ltd.

Om nucleic - nucleic search, using bw model
 Run on: February 5, 2006, 10:56:01 ; Search time 72 Seconds
 (without alignments)
 469.079 Million cell updates/sec

Title: US-10-761-557-4
 Perfect score: 19
 Sequence: 1 ggcagtgtgagccaaac 19

Scoring table: OLIGO NUC
 Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 19

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:
 1: /cgm2_6/pcodata/1/ina/1 COMB .seq:/*
 2: /cgm2_6/pcodata/1/ina/5 COMB .seq:/*
 3: /cgm2_6/pcodata/1/ina/6 COMB .seq:/*
 4: /cgm2_6/pcodata/1/ina/6B COMB .seq:/*
 5: /cgm2_6/pcodata/1/ina/H COMB .seq:/*
 6: /cgm2_6/pcodata/1/ina/PICTUS COMB .seq:/*
 7: /cgm2_6/pcodata/1/ina/PP COMB .seq:/*
 8: /cgm2_6/pcodata/1/ina/RE COMB .seq:/*
 9: /cgm2_6/pcodata/1/ina/backfile1.seq:/*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
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No matches found

Search completed: February 5, 2006, 12:04:00
 Job time : 72 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 5, 2006, 11:21:57 i Search time 344.5 Seconds

(without alignments) 456.076 Million cell updates/sec

Title: US-10-761-557-4

Perfect score: 19

Sequence: 1 ggcagtgttagccgaaac 19

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 19

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Published Applications_NA_Main: *
 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq: *
 2: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq: *
 3: /cgn2_6/podata/1/pubpna/US09_PUBCOMB.seq: *
 4: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq: *
 5: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq: *
 6: /cgn2_6/podata/1/pubpna/US10B_PUBCOMB.seq: *
 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq: *
 8: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq: *
 9: /cgn2_6/podata/1/pubpna/US10E_PUBCOMB.seq: *
 10: /cgn2_6/prodata/1/pubpna/US11_PUBCOMB.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	19	100.0	19 8 US-10-761-557-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
 US-10-761-557-4 Application US/10761557
 Sequence 4 Application US/10761557
 Publication No. US20040220082A1
 GENERAL INFORMATION:
 APPLICANT: Surmeier, D. James
 APPLICANT: Tkatch, Tatiana
 APPLICANT: Baranaukas, Gytis
 TITLE OF INVENTION: Manipulation of Neuronal Ion Channels
 FILE REFERENCE: NWESTRN-08739
 CURRENT APPLICATION NUMBER: US/10/761,557
 CURRENT FILING DATE: 2004-01-21
 NUMBER OF SEQ ID NOS: 5
 SOFTWARE: Patentin version 3.2
 SEQ ID NO 4
 LENGTH: 19
 TYPE: DNA

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: February 5, 2006, 11:31:41 ; Search time 184 Seconds
(without alignments)

86.540 Million cell updates/sec

Title: US-10-761-557-4
Perfect score: 19
Sequence: 1 ggcagtgtggccgaaac 19

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 6068529 seqs, 419036697 residues

Word size : 19
Total number of hits satisfying chosen parameters: 0
Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Listing first 100 summaries

Database : Published_Applications_NA_New.*
1: /cgn2_6/ptodata/2/pubpna/us08_NEW_PUB.seq;*
2: /cgn2_6/ptodata/2/pubpna/us06_NEW_PUB.seq;*
3: /cgn2_6/ptodata/2/pubpna/us07_NEW_PUB.seq;*
4: /cgn2_6/ptodata/2/pubpna/pct_NEW_PUB.seq;*
5: /cgn2_6/ptodata/2/pubpna/us05_NEW_PUB.seq;*
6: /cgn2_6/ptodata/2/pubpna/us10_NEW_PUB.seq;*
7: /cgn2_6/ptodata/2/pubpna/us10_NEW_PUB.seq1;*
8: /cgn2_6/ptodata/2/pubpna/us11_NEW_PUB.seq;*
9: /cgn2_6/ptodata/2/pubpna/us11_NEW_PUB.seq2;*
10: /cgn2_6/ptodata/2/pubpna/us11_NEW_PUB.seq3;*
11: /cgn2_6/ptodata/2/pubpna/us60_NEW_PUB.seq;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match Length	DB ID	Description
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No matches found

Search completed: February 5, 2006, 13:13:41
Job time : 184 secs

LOCUS	RRPCP2858	2858 bp	mRNA	linear	ROD 14 -JAN-1993
DEFINITION	R.rattus mRNA for potassium channel protein	(2858 bp).			
ACCESSION	X62841				
VERSION	X62841.1	GI:57648			
KEYWORDS	voltage-gated potassium channel.				
ORGANISM	Rattus rattus	(black rat)			
SOURCE	Rattus rattus				
REFERENCE	1	(bases 1 to 2858)			
AUTHORS	Reitig, J., Wunder, F., Stocker, M., Lichtenhagen, R., Mastiaux, F., Bech, S., Kues, W., Pedarzani, P., Schroeter, K.H., Ruppertsberg, J.P., Veh, R. and Pongs, O.				
TITLE	Characterization of a Shaw-related potassium channel family in rat brain				
JOURNAL	EMBO J.	11 (7), 2473-2486 (1992)			
PUBMED	1373392				
REFERENCE	2 (bases 1 to 2858)				
AUTHORS	Pongs, O.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-OCT-1991) O. Pongs, Zentrum f Molekulare Neurobiologie, ZMHH Haus 42, Martinistr 52, 2000 Hamburg 20, FRG Location/Qualifiers				
FEATURES					

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LOCUS RRPCCP2858 2858 bp mRNA linear ROD 14-JAN-1993

DEFINITION R.rattus mRNA for potassium channel protein (2858 bp).

VERSION X62841

KEYWORDS X62841..1 GI:57648

SOURCE Rattus rattus (black rat)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurocapthi; Muroidea; Muridae; Murine; Rattus.

REFERENCE 1 (bases 1 to 2858)

AUTHORS Retting, J., Wunder, F., Stocker, M., Lichtenhagen, R., Mastiaux, F., Beck, S., Kues, W., Pedarzani, P., Schroeer, K.H., Ruppertsberg, J.P., Veh, R. and Pongs, O.

TITLE Characterization of a Shaw-related potassium channel family in rat brain

JOURNAL EMBO J. 11 (7), 2473-2486 (1992)

PUBLMED 1378392

REFERENCE 2 (bases 1 to 2858)

AUTHORS Pongs, O.

TITLE Direct Submission (22-OCT-1991) O. Pongs, Zentrum f Molekulare Neurobiologie, ZMNH Haus 42, Martinistra 52, 2000 Hamburg 20, FRG

JOURNAL

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